



Figure 3

SEQ ID NO: 5 (DNA sequence)

SEQ ID NO: 6 (Protein sequence)

aaataaat ataatatag ttttaagtaa aaatttcga aaaaatgtg atttcgttg	60	gaa gag gaa att ggc cct gtt cca cca aaa acc gaa acg cct gat ggc	900
aaatgcgaa gcgtctctt cgaagaagca gctatttca atatttcgc gatttgaaa	120	Glu Glu Glu Ile Gly Pro Val Pro Lys Thr Lys Thr Pro Asp Gly	240
gtcgaagca agaatcaatc tttttcggc ttattttcat cattttatg gattgtctt	180	225 230 235	
atg ttg aat aaa gca ggc att gca gag ccg agc ttg tgg act cgt gcg	228	gct cgc tat tgt gct gct att ggt att gca cag gcc ctt aat gaa	948
Met Leu Asn Lys Ala Gly Ile Ala Glu Pro Ser Leu Trp Thr Arg Ala	1	Ala Arg Tyr Cys Ala Ala Ile Gly Ile Ala Gln Ala Leu Asn Glu	
1 5 10 15		245 250 255	
gat gct atg aaa gtg cat acc gat gat ccc ccg gca acc atg cct acc	276	gcc cgc acc gaa tgg aaa ttg tta ccg cct ttg gta acc gcc ttt ggt	996
Asp Ala Met Lys Val His Thr Asp Asp Pro Thr Ala Thr Met Pro Thr	20 25 30	Ala Arg Thr Glu Trp Lys Leu Leu Pro Pro Leu Val Thr Ala Phe Gly	
20 25 30		260 265 270	
att gat tat gac ttt cct gtc atg act gat aaa tat tgg gtt tgg gac	324	gtc aat gac cag acg gag ccg cct cat gtc gtt ttc cag aat ggc ttg	1044
Ile Asp Tyr Asp Phe Pro Val Met Thr Asp Lys Tyr Trp Val Trp Asp	35 40 45	Val Asn Asp Gln Thr Glu Arg Pro His Val Val Phe Gln Asn Gly Leu	
35 40 45		275 280 285	
act tgg ccc tta cgc gat att aac ggt cag gtt gtc agc ttc caa ggt	372	acc tat ctc ttt acg atc agt cat cat tcy act tat gcc gat ggt ttg	1092
Thr Trp Pro Leu Arg Asp Ile Asn Gly Gln Val Val Ser Phe Gln Gly	50 55 60	Thr Tyr Leu Phe Thr Ile Ser His His Ser Thr Tyr Ala Asp Gly Leu	
50 55 60		290 295 300	
tgg tgc gtg atc ttt gtt ttg gtc gct gat cgc acc aaa tat ggt tgg	420	tcg ggt cct gat ggg gtt tat ggc ttt gtt tct gaa aac ggc att ttt	1140
Trp Ser Val Ile Phe Ala Leu Val Ala Asp Arg Thr Lys Tyr Gly Trp	65 70 75	Ser Gly Pro Asp Gly Val Tyr Gly Phe Val Ser Glu Asn Gly Ile Phe	
65 70 75		305 310 315	
cat aat cgc aat gat ggc gcc aga att ggt tat ttc tat tca cgt ggt	468	ggc cct tat gaa ccg cgt aat ggt tcc ggt ttg gtt ctc ggt aac ccc	1188
His Asn Arg Asn Asp Gly Ala Arg Ile Gly Tyr Phe Tyr Ser Arg Gly	85 90 95	Gly Pro Tyr Glu Pro Leu Asn Gly Ser Gly Leu Val Leu Gly Asn Pro	
85 90 95		325 330 335	
gga agc aac tgg att ttt ggt ggt cat ctt ctg aaa gat ggt gcc aat	516	tct tca cag cct tat cag gct tat tcc cat tat gat atg aca aat ggg	1236
Gly Ser Asn Trp Ile Phe Gly Gly His Leu Leu Lys Asp Gly Ala Asn	100 105 110	Ser Ser Gln Pro Tyr Gln Ala Tyr Ser His Tyr Val Met Thr Asn Gly	
100 105 110		340 345 350	
ccg cgt tct tgg gaa tgg tct ggt tgc agc att atg gca ccg ggt acg	564	ctg gtg acc tcc ttc att gat acc att ccg agt tct gac ccg aat gtc	1284
Pro Arg Ser Trp Glu Trp Ser Gly Cys Thr Ile Met Ala Pro Gly Thr	115 120 125	Leu Val Thr Ser Phe Ile Asp Thr Ile Pro Ser Ser Asp Pro Asn Val	
115 120 125		355 360 365	
gcc aat tct gtc gaa gta ttc ttt acg tct gtc aat gat acg ccg tca	612	tat cgt tat ggt ggc acc ttg gca ccg acc atc aaa ttg gaa ttg gtt	1332
Ala Asn Ser Val Glu Val Phe Phe Thr Ser Val Asn Asp Thr Pro Ser	130 135 140	Tyr Arg Tyr Gly Gly Thr Leu Ala Pro Thr Ile Lys Leu Glu Leu Val	
130 135 140		370 375 380	
gaa tcc gtt cct gcc cag tgc aag ggc tac atc tat gcc gat gat aaa	660	ggc cat cgc agc ttc gtt acc gaa gtg aag ggt tat ggc tat att ccg	1380
Glu Ser Val Pro Ala Gln Cys Lys Gly Tyr Ile Tyr Ala Asp Asp Lys	145 150 155	Gly His Arg Ser Phe Val Thr Glu Val Lys Gly Tyr Gly Tyr Ile Pro	
145 150 155		385 390 395	
tcg gta tgg ttt gac ggt ttt gat aaa gtg acc gat ctg ttt cag gca	708	cca cag atc gag tgg ttg gca gaa gat gaa tct tct aat tct gcg gca	1428
Ser Val Trp Phe Asp Gly Phe Asp Lys Val Thr Asp Leu Phe Gln Ala	165 170 175	Pro Gln Ile Glu Trp Leu Ala Glu Asp Glu Ser Ser Asn Ser Ala Ala	
165 170 175		405 410 415	
gat ggc ctt tat tat gct gat tat gca gaa aat aat ttc tgg gat ttc	756	gcc ctc tct tta ttg aat aaa taagatttat tcaattgaaa tgaagtctct	1479
Asp Gly Leu Tyr Tyr Ala Asp Tyr Ala Glu Asn Asn Phe Trp Asp Phe	180 185 190	Ala Leu Ser Leu Leu Asn Lys	
180 185 190		420	
cgc gat ccg cat gtc ttc att acc ccg aag ata ggc aaa aca tat gcc	804	gattatgctt gaataagca ttatcatctt ttgagttcat ttcaacttaa ggggtcatcag	1539
Arg Asp Pro His Val Phe Ile Thr Pro Lys Ile Gly Lys Thr Tyr Ala	195 200 205	ggcatttgc cctgagaca ccttctctat tcttaataat aattcaaga aagtgatat	1599
195 200 205		tacttaaat gtttaatttt aatgcagtc gctggacgcg agcccaagcg atgaagtga	1659
ttg ttt gaa ggt aat gtt gcc atg gag cgc ggt acc gtc gct gtt ggc	852	ataaattga tttagcacc tctatgcgg aatcggcac tgatttccc attatcgctg	1719
Leu Phe Glu Gly Asn Val Ala Met Glu Arg Gly Thr Val Ala Val Gly	210 215 220	atgacttgcg gctgaggat acttggccat taaggccat caatggcaat cctgtcagct	1779
210 215 220		ttaaaggctg gaattgattt t	